

On page 9, lines 25-32 and page 10, lines 1-2 please substitute the existing paragraph with the following paragraph:

In a preferred embodiment, breast cancer sequences are those that are up-regulated in breast cancer; that is, the expression of these genes is higher in carcinoma as compared to normal breast tissue. "Up-regulation as used herein means at least about a 50% increase, preferably a two-fold change, more preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see e.g., Benson, DA et al., Nucleic Acids Research 26:1-7 (1998). In addition, these genes were found to be expressed in a limited amount or not at all in bladder, bone marrow, brain, colon, heart, kidney, liver, lung, muscle, pancreas, salivary gland, skin, small intestine, spinal cord, spleen,, stomach, thymus and uterus.

On page 13, lines 24-33 and page 14, lines 1-3 please replace the existing paragraph with the following paragraph:

Another example of a useful algorithm is the BLAST algorithm, described in Atschul et al., J. Mol. Biol. 215, 403-410 (1990) and Karlin et al., PNAS USA 90:5873-5787 (1993). A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Atschul et al., Methods in Enzymology, 266:460-480 (1996). WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and the composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of